

**Amendments to the Claims:**

This listing of claims will replace all prior versions, and listings, of claims in the application:

**Listing of Claims:**

Claim 25 (currently amended): A vaccine composition which comprises:[[-]]

(a) antigenic material selected from:

(i) an attenuated live mutant bacterium having a genome wherein a native gene having a function of ferric uptake regulation (*fur* gene) has been modified by mutation whereby expression of a gene product corresponding to said *fur* gene is regulated independently of the iron concentration in the environment of the bacterium; and

(ii) a non-viable preparation comprising bacterial membrane antigens from cultured cells of a mutant bacterium having a genome wherein a native gene having a function of ferric uptake regulation (*fur* gene) has been modified by mutation whereby expression of a gene product corresponding to said *fur* gene is regulated independently of the iron concentration in the environment of the bacterium;

together with:[-]]

(b) a pharmaceutically acceptable diluent or carrier.

Claim 26 (original): The vaccine composition of claim 25, wherein said mutant bacterium comprises *Neisseria meningitidis*, *Neisseria gonorrhoeae*, *Helicobacter pylori*, *Salmonella typhi*, *Salmonella typhimurium*, or *E. coli*.

Claim 27 (original): The vaccine composition of claim 25, wherein said non-viable preparation comprising bacterial membrane antigens is obtained by isolating bacterial membrane vesicles from said cultured cells of said mutant bacterium.

Claim 28 (original): An attenuated mutant bacterium having a genome wherein a native fur gene, having a function of ferric uptake regulation, has been modified by mutation whereby expression of a gene product corresponding to said fur gene is regulated independently of the iron concentration in the environment of the bacterium.

Claim 29 (original): The attenuated mutant bacterium of claim 28 which is a gram-negative bacterium.

Claim 30 (original): The attenuated mutant bacterium of claim 28, wherein the mutant bacterium comprises a *Neisseria meningitidis*, *Neisseria gonorrhoeae*, *Helicobacter pylori*, *Salmonella typhi*, *Salmonella typhimurium*, enteropathogenic *E. coli* (EPEC), enteroinvasive *E. coli* (EIEC), enterotoxigenic *E. coli* (ETEC), enterohaemorrhagic *E. coli* (EHEC), verotoxigenic *E. coli* (VTEC), *Vibrio cholerae*, *Shigella* spp., *Haemophilus influenzae*, *Bordetella pertussis* or *Pseudomonas aeruginosa* species.

Claim 31 (original): The attenuated mutant bacterium of claim 28, wherein the mutant bacterium comprises a *Neisseria meningitidis* or *Neisseria gonorrhoeae* species.

Claims 32 (original): The attenuated mutant bacterium of claim 28, which has a mutation of a gene essential for production of a bacterial metabolite or catabolite not produced by a human or animal.

Claim 33 (original): The attenuated mutant bacterium of claim 28, which has an attenuating mutation of a gene selected from aro, asd, pur and pyr genes.

Claim 34 (original): The attenuated mutant bacterium of claim 33, wherein said mutation is of a gene selected from aroA, aroB, aroC, aroD, aroL, purA, purB, purE, pyrA, pyrB and pyrE.

Claim 35 (original): The attenuated mutant bacterium of claim 28, which has a recA mutation.

Claim 36 (original): The attenuated mutant bacterium of claim 28, which has a mutation by which expression of a toxin gene has been modified or eliminated.

Claim 37 (original): The attenuated mutant bacterium of claim 28, which has a mutation at a site homologous to the *E. coli* minB locus.

Claim 38 (original): The attenuated mutant bacterium of claim 28, which has a mutation in a gene involved in uptake of DNA.

Claim 39 (original): The attenuated mutant bacterium of claim 38, which is of a species selected from *N. meningitidis* and *N. gonorrhoeae*, and wherein said mutation in said gene involved in uptake of DNA is a comA mutation.

Claim 40 (original): The attenuated mutant bacterium of claim 28, which is of a species selected from *N. meningitidis* or *N. gonorrhoeae* and which has a mutation in the galE gene.

Claim 41 (original): The attenuated mutant bacterium of claim 40, which further has a mutation in the opc gene to modify or eliminate expression of opc protein.

Claim 42 (original): An attenuated mutant bacterial strain of the species *N. meningitidis* which has a genotype selected from:

- (a) mutation of aroB, lac:fur fusion, and mutation of recA;
- (b) mutation of aroB, mutation of galE, lac:fur fusion, and mutation of recA;
- (c) mutation of aroL, lac:fur fusion, and mutation of recA; and
- (d) mutation of aroL, mutation of galE, lac:fur fusion, and mutation of recA.

Claim 43 (original): The attenuated mutant bacterial strain of the species *N. meningitidis*, according to claim 42, which also has at least one characteristic selected from: a minB mutation; an RTX negative phenotype; and an opc gene mutation whereby expression of said opc gene has been modified or eliminated.

Claim 44 (original): A preparation of membrane vesicles obtained by isolating bacterial membrane vesicles from cultured cells of a mutant bacterium having a genome wherein a native fur gene having a function of ferric uptake regulation has been modified by mutation whereby expression of a gene product corresponding to said fur gene is regulated independently of the iron concentration in the environment of the bacterium.

Claim 45 (original): A method of treating a subject which is a human or non-human animal, said method comprising vaccinating said subject with the vaccine composition of claim 25 thereby to stimulate an immune response against said bacterium.

Claims 46-48 (canceled).